

I. AMENDMENTS

A. In the Specification

Please amend the Title of the application at page 1 and page 142, as follows:

USE OF FOLLISTATIN TO INCREASE MUSCLE MASS TRANSGENIC NON-HUMAN ANIMALS EXPRESSING A TRUNCATED ACTIVIN TYPE II RECEPTOR

Please amend the following paragraphs of the specification, as indicated:

[0035] A number of genome databases are available for comparison, including, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, at hypertext transfer protocol ("http"), URL "weber.u.Washington.edu/~roach/human_genome_progress2.html" http://weber.u.Washington.edu/~roach/human_genome_progress-2.html). In addition, at least twenty-one genomes have been sequenced in their entirety, including, for example, M. genitalium, M. jannaschii, H. influenzae, E. coli, yeast (S. cerevisiae), and D. melanogaster. Significant progress has also been made in sequencing the genomes of model organism such as mouse, C. elegans, and Arabadopsis sp. Several databases containing genomic information annotated with some functional information are maintained by different organizations, and are accessible via the internet, for example, at http, URL "www.tigr.org/tdb"; at http, on the world wide web ("www"), at URL "genetics.wisc.edu"; at http, URL "genome-www.stanford.edu/~ball"; at http "hiv-web.lanl.gov"; at http, on the www, at URL "ncbi.nlm.nih.gov"; at http, on the www, at URL "ebi.ac.uk"; at http, URL "Pasteur.fr/other/biology"; and at http, on the www, at URL "genome.wi.mit.edu" http://www.tigr.org/tdb; http://www.genetics.wisc.edu; http://genome-www.stanford.edu/~ball; http://hiv-web.lanl.gov; http://www.ncbi.nlm.nih.gov; http://www.ebi.ac.uk; http://Pasteur.fr/other/biology; and http://www.genome.wi.mit.edu.

[0036] One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described by Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1977; J. Mol. Biol. 215:403-410, 1990, each of which is incorporated herein by reference). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (at http, on the www, at URL "ncbi.nlm.nih.gov" ~~http://www.ncbi.nlm.nih.gov~~).

[0039] The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (i.e., aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993, each of which is incorporated herein by reference). Less preferably, the PAM or PAM250 matrices may also be used (Schwartz and Dayhoff, eds., "Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure" (Washington, National Biomedical Research Foundation 1978)). BLAST programs are accessible through the U.S. National Library of Medicine, for example, at http, on the www, at URL "ncbi.nlm.nih.gov" ~~http://www.ncbi.nlm.nih.gov~~.